Spectral analysis for gene communities in cancer cells

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Supplementary File

Title: Spectral analysis for gene communities in cancer cells

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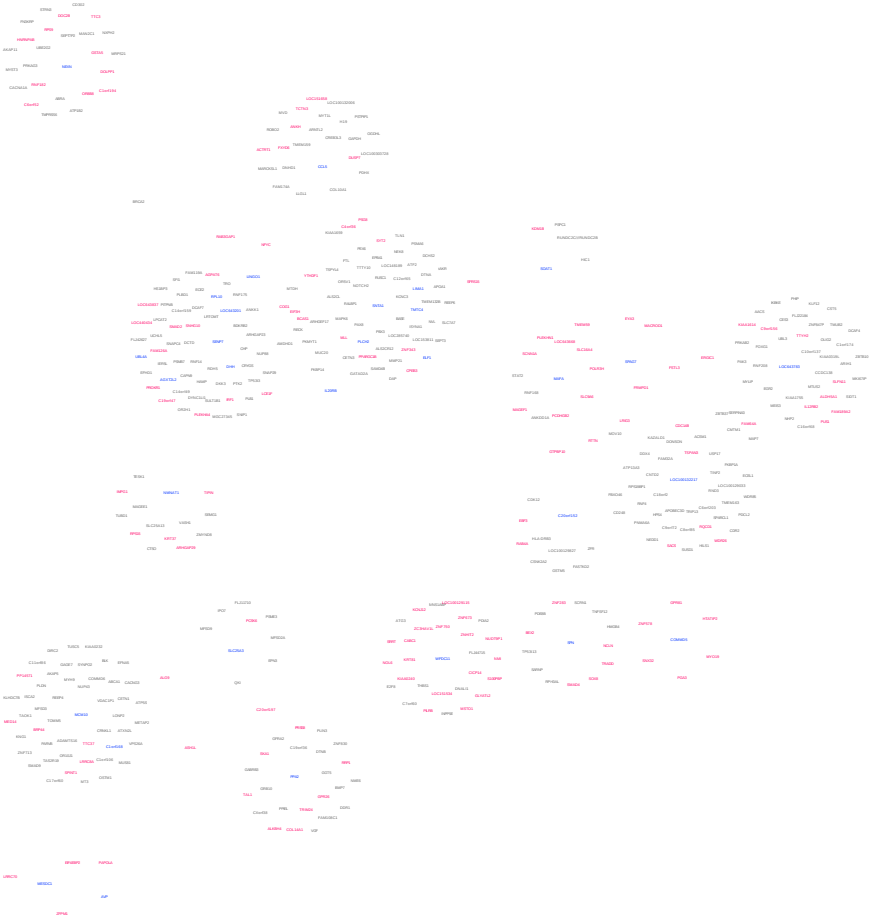
Supplementary Figures 1-3 are deposited in the public website: “NDEx-The Network Data Exchange.” URL: https://home.ndexbio.org/index/

Supplementary Figure 1



Supplementary Figure 1 caption:

A network graph for the sub-network of the gene interaction network in colon cancer. The extracted edges which have $\Delta > 25$ are shown, where Δ is the node degree discrepancy. The node attribute ‘Degree’ in this graph shows the node degree k in the original network before the extraction of the edges. Node sizes are proportional to k and node colors are dependent of k. The node labels are gene names and the label colors are purple for k=1node, red for nodes which have $2 \leqq k \leqq 6$, blue for nodes $k \geqq 25$, and gray for $6<k<25$ nodes.

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Supplementary Figure 2

Supplementary Figure 2 caption:
A network graph for the sub-network of the gene interaction network in colorectal cancer (ID:125). The disassortative communities which have edges $\Delta > 25$ are shown, where Δ is the node degree discrepancy. The node color and the node size are the same as in Suppl. Fig. 1.
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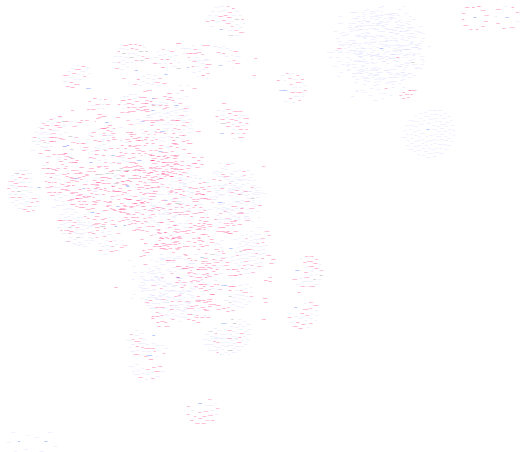
Supplementary Figure 3



Supplementary Figure 3 caption:
A network graph for the sub-network of the gene interaction network in breast cancer (ID:248). The disassortative communities which have edges $\Delta > 25$ are shown, where Δ is the node degree discrepancy. The node color and the node size are the same as in Suppl. Fig. 1.
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